



923.1.TXT

SEQUENCE LISTING

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<120> CRYSTALLINE FORM OF FATTY ACID AMIDE  
HYDROLASE (FAAH)

<130> 923.1

<140> US 10/534,766

<141> 2005-05-12

<150> PCT/US03/036125

<151> 2003-11-14

<150> US 60/425,788

<151> 2002-11-14

<160> 1

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 579

<212> PRT

<213> Homo sapiens

<400> 1

Met	Val	Leu	Ser	Glu	Val	Trp	Thr	Thr	Leu	Ser	Gly	Val	Ser	Gly	Val
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Cys	Leu	Ala	Cys	Ser	Leu	Leu	Ser	Ala	Ala	Val	Val	Leu	Arg	Trp	Thr
			20					25					30		
Gly	Arg	Gln	Lys	Ala	Arg	Gly	Ala	Ala	Thr	Arg	Ala	Arg	Gln	Lys	Gln
	35					40					45				
Arg	Ala	Ser	Leu	Glu	Thr	Met	Asp	Lys	Ala	Val	Gln	Arg	Phe	Arg	Leu
	50					55					60				
Gln	Asn	Pro	Asp	Leu	Asp	Ser	Glu	Ala	Leu	Leu	Thr	Leu	Pro	Leu	Leu
65				70					75					80	
Gln	Leu	Val	Gln	Lys	Leu	Gln	Ser	Gly	Glu	Leu	Ser	Pro	Glu	Ala	Val
			85						90					95	
Phe	Phe	Thr	Tyr	Leu	Gly	Lys	Ala	Trp	Glu	Val	Asn	Lys	Gly	Thr	Asn
			100					105					110		
Cys	Val	Thr	Ser	Tyr	Leu	Thr	Asp	Cys	Glu	Thr	Gln	Leu	Ser	Gln	Ala
			115				120					125			
Pro	Arg	Gln	Gly	Leu	Leu	Tyr	Gly	Val	Pro	Val	Ser	Leu	Lys	Glu	Cys
	130					135					140				
Phe	Ser	Tyr	Lys	Gly	His	Asp	Ser	Thr	Leu	Gly	Leu	Ser	Leu	Asn	Glu
145					150					155					160
Gly	Met	Pro	Ser	Glu	Ser	Asp	Cys	Val	Val	Val	Gln	Val	Leu	Lys	Leu
			165						170					175	
Gln	Gly	Ala	Val	Pro	Phe	Val	His	Thr	Asn	Val	Pro	Gln	Ser	Met	Leu
			180					185					190		
Ser	Phe	Asp	Cys	Ser	Asn	Pro	Leu	Phe	Gly	Gln	Thr	Met	Asn	Pro	Trp
	195					200						205			
Lys	Ser	Ser	Lys	Ser	Pro	Gly	Gly	Ser	Ser	Gly	Gly	Glu	Gly	Ala	Leu

## 923.1.TXT

210		215		220	
Ile Gly Ser Gly Gly Ser Pro Leu Gly Leu Gly Thr Asp Ile Gly Gly					
225		230		235	240
Ser Ile Arg Phe Pro Ser Ala Phe Cys Gly Ile Cys Gly Leu Lys Pro					
	245		250		255
Thr Gly Asn Arg Leu Ser Lys Ser Gly Leu Lys Gly Cys Val Tyr Gly					
	260		265		270
Gln Thr Ala Val Gln Leu Ser Leu Gly Pro Met Ala Arg Asp Val Glu					
	275		280		285
Ser Leu Ala Leu Cys Leu Lys Ala Leu Leu Cys Glu His Leu Phe Thr					
	290		295		300
Leu Asp Pro Thr Val Pro Pro Leu Pro Phe Arg Glu Glu Val Tyr Arg					
305		310		315	320
Ser Ser Arg Pro Leu Arg Val Gly Tyr Tyr Glu Thr Asp Asn Tyr Thr					
	325		330		335
Met Pro Ser Pro Ala Met Arg Arg Ala Leu Ile Glu Thr Lys Gln Arg					
	340		345		350
Leu Glu Ala Ala Gly His Thr Leu Ile Pro Phe Leu Pro Asn Asn Ile					
	355		360		365
Pro Tyr Ala Leu Glu Val Leu Ser Ala Gly Gly Leu Phe Ser Asp Gly					
	370		375		380
Gly Arg Ser Phe Leu Gln Asn Phe Lys Gly Asp Phe Val Asp Pro Cys					
385		390		395	400
Leu Gly Asp Leu Ile Leu Ile Leu Arg Leu Pro Ser Trp Phe Lys Arg					
	405		410		415
Leu Leu Ser Leu Leu Leu Lys Pro Leu Phe Pro Arg Leu Ala Ala Phe					
	420		425		430
Leu Asn Ser Met Arg Pro Arg Ser Ala Glu Lys Leu Trp Lys Leu Gln					
	435		440		445
His Glu Ile Glu Met Tyr Arg Gln Ser Val Ile Ala Gln Trp Lys Ala					
	450		455		460
Met Asn Leu Asp Val Leu Leu Thr Pro Met Leu Gly Pro Ala Leu Asp					
465		470		475	480
Leu Asn Thr Pro Gly Arg Ala Thr Gly Ala Ile Ser Tyr Thr Val Leu					
	485		490		495
Tyr Asn Cys Leu Asp Phe Pro Ala Gly Val Val Pro Val Thr Thr Val					
	500		505		510
Thr Ala Glu Asp Asp Ala Gln Met Glu Leu Tyr Lys Gly Tyr Phe Gly					
	515		520		525
Asp Ile Trp Asp Ile Ile Leu Lys Lys Ala Met Lys Asn Ser Val Gly					
	530		535		540
Leu Pro Val Ala Val Gln Cys Val Ala Leu Pro Trp Gln Glu Glu Leu					
545		550		555	560
Cys Leu Arg Phe Met Arg Glu Val Glu Gln Leu Met Thr Pro Gln Lys					
	565		570		575
Gln Pro Ser					